The Dictyostelium homologue of mammalian soluble adenylyl cyclase encodes a guanylyl cyclase

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Alignment of the sCKH region

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DdsGC 1473 GIIGRHTQLR-QMANIIDQITSNSGPTHVAIIEAEAGLGKSRLISEIKYSFCMDLKMFKASGI-QMSESISFYI
HssAC1 485 PLLGRNKEINYFMYTMKKFLISN--SSQVLMYEGLPGYGKSQILMKIEYLAQGKNHRIIA--I-SLNK-ISFH-
AsKin  298 KLYGREAEIDILMAAFENVNQGH---KELILVAGYSGIGKSALVNEIHKPVIKNRGYFIAGKFEQFQRNIPY--
MlsAC  287 TLVGREWELA-TLAAMLDRSIG--GRGSVVGLVGPAGIGKTRLVAEAVQLAKGLEVEVFS--V--FCESHATDV

DdsGC 1545 WKQILLQFLKDESINGYQSFSDFNFTQ-IQLLNQ---VLD[16]KLPIVEQNQLQTSVIKLTSEELKENRRYSA
HssAC1 552 QTFYTIQMFMAN-VLGLDTCKHYKERQ-TNLRNKVMTLLDEKF-YCLLNDIFHVQFP-ISREISRMSTLKK---
AsKin  367 --ASLIQAFQ----ELMQQLLTESGQQLANWRERILAALVPNA--QIIIDVIPELELIIGKQPEV-PQLGSAEA
MlsAC  354 AFDVVAQLVR----AVAQISGLDDRSARARVREQIPDADTQD---LLLLDDLLGIADPAVELPRLDPDARRRR-

DdsGC 1622 QQRAESLQL--TMMKILTKAIPTGS--II-VIDDAQFMDSASWTLTLNAVKNLAN--CLIIISLRPSKDGIPYG
HssAC1 619 -QK----QLEILFMKILKLIVKEE--RIIFIIDEAQFVDSTSWRFMEKLIRTLP---IFIIMSLCP-FVNIPCA
AsKin  432 -QN--RFNL--VMQKFINVFAQKEHPLVVF-LDDLQWADLASLKLIQLLAINSDIQYLFLIGAYRDNEVDSSHH
MlsAC  420 -----LTAL-------INVAQLALSRPAVFVVEDVHWIDEVSDSMLADFLAVIPQTRSMALVTYRPEYHGALRH

DdsGC 1694 FSQLPTELVTKIQLEPLNG---KVETTLLV-E----------RMLDFPSDE-S-GIP---DEIIE--EIYNRS
HssAC1 682 AA----RAVIK-NRNTTYIVVGAVQPNDISNKICLDLNVSCISKELDSYLGEGSCGIPFYCEELLKNLEHHEVL
AsKin  500 LMLILQEI-EK-NRTPINIIYCQ---N---LKIT-D-----VCQ-LVGDTLK-S-GLED-SKELAKLIFHKTG-
MlsAC  482 VVGAQIIAVA-----PL----SDVETSTLVAEL-LGLDQS-VTQIGELITER-AAGNPFFAQEITR--ELAERG

DdsGC 1746 QGNHFVIEEM--VKWSN-FKWTNRMKHL---------QDSLILKRQFDHVR---LSLPPT---VTSLITSRVDR
HssAC1 751 VFQQTESEEKTNRTWNNLFKYSIKLTEKLNMVTLHSDKESEEVCHLTSGVRLKNLS-PPTSLKEISLIQLDSMR
AsKin  555 ---GNPFFINQLLKFIHQENLLVFNFITGQWQWYIQY----------------IQMLDITDNVVDLMIGKIQK
MlsAC  542 -------------------------VLTGERGRYACSTD--------------VAEVCVPATLQATIAARIDR

DdsGC 1801 LSP-IQQLELKI-ASVIGMPFTVDSLHRILPLDAISKQDLAKDLAVL-ERLDFIKS[17]QLQKQLLNNQADHSS
HssAC1 824 LS---HQMLVRC-AAIIGLTFTTELIFEILPC-WNMKM-MIKTLATLVESNIFYCFRNGKELQKAL--KQNDPSF
AsKin  609 L-KDNTQNIIKI-AACIGNRFNLNTLSCI-----NEK----------SHNATALDIWEALQAGLII-------
MlsAC  576 LSPPAKQLLV-A-AAVLGFRFGSDLLASLG-------------------------------------------

DdsGC 1886 YKTNNVLLLASQP---[22]EQPSTPTSIINNNLLYSFHHTRTQEVIYDLMLFSQRRELHQKIAK-VLEDT--C
HssAC1 891 EVHYRSLSLKPSEGMDHGEEEQLRELENEVIECHRIRFCNPMMQKTAYELWLKDQRKAMHLKCARFLEEDAHRC
AsKin  658 ------------PLSDNYKLPQLLDDVDIFV--IDYKFLHDRVQQAAYALIPDEHKKEIHLNIGRLLLKNIDKS
MlsAC  604 ------IDLSVDELIDANLVDQVR-----FTAPVEYAFRHPLIRTVAYESQLKSDRARLHRRLAA-AIEARAPH

DdsGC 1972 -TPQHSLFTSLVHHYHSAQNNSKTIEYATKAGVLAQAENNNKEAIKFFQLALKCMEQEFIAEEEVKIHKKLHRR
HssAC1 965 DHCRGRDFIPYHHFTVNIRLNALDMDAIKKMAMSHGFKTEEKLILSNSEIPETSAFFPENRSPEEIREKILNF-
AsKin  718 LLEEKIFDIA-NQLNMGAGLITAPEERYKLAALNLMAGRKAKDST-AYESAVSFLKQGLNLLDIDCWQKHYEL-
MlsAC  666 SVDQHAVLIA-EH-LEAAGDLHAAYGWHMRAAAWA-TNQDVRAARVSWEHATKIADALT-AEDPHRAAMCIAPR

DdsGC 2045 S[114]PPTLADLVSLGFKKVPIEIISITRKLGLAL-F-NVGRFRQASYHLLNALKYLGLEPPTPKDYSSGASK
HssAC11038 FDHVLTKMKTSDEDIIPLESCQCEEILEIVILPLAHHFLALGENDKALYYFLEIASAYLIFCDNYMAYMYLNEG
AsKin  789 ----------TLDLHVETVESAYLNTNFEEAEPL---------FATVIANSKNILDAVKVYEKKIQFYVGQN--
MlsAC  736 TRLCGIAWRGRFNSSSGFDEVRQLCNATGDKAPLAV--ATVGPAIDHVYQDRLH 787[stop]
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DdsGC 2226 PKLRTLAKA-----AVRQDSATKFFSCNLDMLEKREAILCLFVQSKISLHDCSKTLDSWCSYVSLQLS-FDNSH
HssAC11112 QKLLKTLKKD-KSWSQTFESAT-FYS--LK-GEVCFNMG-QIVLAKKMLRKALKLLNRIFPYN-L-ISLFLHIH
AsKin  842 -RMREALDLDLQVLGMLGVSLSQTPPAELKIEELIN-LPEMMDPSKLAAMR-ILMTAMPPAYLAADPALLPLIA

DdsGC 2294 SSIKNRLFNSLG[39]------------------------VQTSLT------DWNLQAEAYSIGIRVLGNNGD
HssAC11178 -VEKNRHFHYVNRQAQESP--------PPGKKRLAQLYRQTVCLSLL-------WRIYSYSYLFHCK--YYAHL
AsKin  912 FTMIDLCLQYGNSSFAAYAYGFYGLILCGPLNNIESGYRF-GKLSLQILNQFNAKEIKSKVYALFN--IFVRHW

DdsGC 2372 SSTPLKYYAEVLSKMDQTNGFVYGNSHQSW-GIYMSGLGRWE-EA-ESGYKKSIEASHKTGDKKLMEESNIFLS
HssAC11234 AVMMQMNTALETQNCFQIIKAYLDYSLYHHLAGYKGVWFKYEVMAMEHIFN-------------LPLKGEGIEI
AsKin  983 KEHIQ--TIEPLQEGVQSGLDTGDIEYVGYNGLLVCWHPFWSGENLETVEQ-----------------------

DdsGC 2443 VCYLLLGSNGGKLSLIYQQTTKALESAR--NRGDNHNQILALTVEGCALFYERQFQRCHTILQDIERLVDLLSI
HssAC11295 VAYVAETLVFNKLIMGHLDLAIELGSRALQMWALLQNPNRHYQSLCRLSRCLLLNSRYPQLIQVLGRLWELSVT
AsKin 1033 --------RLDKYINLAQRIQQEHFTVCL---LILKQLLTELKQGLKNEVYLDGDDFNNSIMQRMAGNITAIFY

DdsGC 2515 KELSNSAHANYTILKAQIAINEKDWQLAYDCCRRVSIIISKCDANNFSMYEAYTGLPLVLIKILQNHQHISATA
HssAC11369 QEHIFSKAFFYFVCLDILLYSGFVYRTFEEC--LEFIHQYENNRILKFHSGLLLGLYSSVAIWYARLQEWDNFY
AsKin 1096 AYLAKSILSYFFKDYSQ-AVKNAELAQQYEVAVG---GTFYLIEYKFYYSLALLALCLNLTSDADITSALEKVS

DdsGC 2589 VTVPKSRLVTE----INDSITILERFAETFPIGQPRLL--LVK---TLMFALGYRESDDQNNLSA-LKEAKEKC
HssAC11441 KFSNRAKNLLP---RRTMTLTYYDGISR-YMEGQVLHLQKQIKEQSENAQASGEELLKNLENLVAQNTTGPVFC
AsKin 1166 ENQQQLKEWADHAPINNQHKYELVEAEKARVLGQVLIAMEYYECAIQGAHKFGYIHEEALAYECA--AEFYFSL

DdsGC 2653 QKLGMSFDFVCIHNPNNNNNNSNNNNSGGSGSPSGNNSPINKRYSVGGIGNYQQANGGQDIKSPVLSPQHSISD
HssAC11611 PRLYHLMAYVCIL------------MGDG--QKCGLFLNTALRLS-ETQGNILEK---CWLNMNKESWYSTSEL
AsKin 1238 GRNEFACLYI-------------TKAHYG-YRHWGASAKVRNLESKYP--ELTAKISSQYPADFTNTNITTSTA

DdsGC 2727 FHYTAADTGTLQPS[86]GAKKDILKKIGIKFWKE 2843[stop]
HssAC11667 KEDQWLQTILSLPSWEKIVAGRVNIQDLQKNKFLMRANTVDNHF 1710[stop]
AsKin 1296 SEKSSGLDLISVIKASQTLSEVILLDNLLEKLMTIVIENAGAQTG


[16]  = INIINNNNNNGNENNE
[17]  = TTINTQQQLLQQLQQQQ
[22]  = NINNNNNNNNNNNNNNNNNAN
[114] = SSQNLKDAVSISSNSNNPNNISFQDLMDSNNSNLVNSNSNNNNSNNNSNNNSNNNS
        LSNLGEDIKDKDKEKEKDKDKEKEKEKEKEKEKEKDKEKDKNNNNNNNNNNNNNNTILN
[39]  = NNNSNNNNNNNNNNNNNNNNNSSNNNELSSSSTTTTTTT
[86]  = VQIGSSRSRPVSVHENVNSSQPLRTVSSQDLSSSSSGSNNSYNGSSDQQSPQSPQSPQSPQSPQSPQSPNSITSQQFSPPNQPSNN
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